Table S2. Significance of Su(H) association in comparison with constrained background model

Comparison of background models after 1000 rounds: DmD8 Twi ChIP data

Displacement of ChIP site (bp)	Su(H)/Twi overlaps	Z-score	*P*-value (random experiments with more overlaps)
1000	177.98	3.09	0.002
2500	152.59	7.13	0*
5000	118.68	11.13	0*
7500	100.98	13.63	0*
10,000	86.57	14.96	0*

By comparison, overlaps in actual dataset=184.

*Highly significant, *P*≤0.001.

Comparison of background models after 1000 rounds: embryonic Twi ChIP data

Displacement of ChIP site (bp)	Su(H)/Twi overlaps	Z-score	*P*-value (random experiments with more overlaps)
1000	67.97	2.13	0.029
2500	62.51	2.89	0.004
5000	55.26	3.92	0*
7500	50.04	4.68	0*
10,000	43.23	6.23	0*
50,000	25.26	11.55	0*
100,000	19.13	14.21	0*

By comparison, overlaps in actual dataset=73.

*Highly significant, *P*≤0.001.